

We Claim:

1. A method for handling a database for bioinformatics, in which a server, which is associated with a database for storing sequence information related with bioinformatics and
5 connected to each user terminal through a specific communication network, compares a sequence requested from each user terminal with sequences of the database to analyze a result of the comparison, the method comprises:

(a) a first step of receiving the sequence from the user terminal to store it in a queue;

10 (b) a second step of checking whether or not there exist other sequences to be compared and analyzed in the queue, simultaneously with the first step;

(c) a third step of reading the sequence of the current order from the database to compare it with all of sequences stored in the queue when there exist other sequences to be compared and analyzed at the second step;

15 (d) a fourth step of judging whether or not there exists a sequence that has been compared and analyzed for all of sequences of the database among the sequences compared and analyzed at the third step, and removing the corresponding sequence from the queue; and,

(e) a fifth step of incrementing the current order by one, initializing the current order when all of the sequences of the database have been read and returning to the second step.

20 2. A recording medium readable by a computer, in which a computer program for executing the first to fifth steps according to claim 1 is recorded.